Mammalian biogeography and the Ebola virus in Africa

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INTRODUCTION

As Ebola virus transmission from wildlife has mostly been linked to people handling and butchering wild animals for bushmeat, it is fundamental to understand how host factors, together with ecological conditions and human behaviour contributes to Ebola virus outbreaks.

Recent biogeographical analyses have highlighted the importance of potential hosts in explaining the spatial assemblage of human infectious diseases worldwide (Murray et al. 2015), but a limited understanding of the animals potentially implicated in the zoonosis has hampered mapping the extent of Ebola virus.

The ecology of the Ebola virus is complex and widely unresolved (Groseth et al. 2007). Thus, imposing restrictions to the selection of animal species considered in a distribution model might underrepresent the zoological substrate that could be determining the virus distribution. Mammalian biodiversity, as a whole, could be the strongest predictor explaining similarities between pathogeographic regions of the world (Murray et al. 2015).

OBJECTIVES

- We analyse the spatial distribution of Ebola virus in Africa, independent of human-to-human transmissions, under the hypothesis that it is influenced by how mammal species are distributed throughout the region.

- We test this hypothesis by verifying whether a distribution model of Ebola virus, based on variables defining the existing types of mammalian distributions in Africa (chorotypes), can better describe the virus occurrences recorded in wildlife than a model based on environmental descriptors alone.

- We propose a way to integrate virological, zoogeographical and environmental information through a combination of biogeographical approaches, and define the areas where Ebola virus may find suitable conditions to occur in the wild.

METHODS

- Favourable areas for Ebola virus were derived from 91 events (**Fig. 1a**): index cases in humans, and virus presence in other mammals (lab detection, or abnormal increase of mortality, **Fig. 2**).
- A model defining environmental favourability for Ebola virus was made by using the Favourability Function (Acevedo & Real 2012), according to variables describing ecosystems, abiotic factors and anthropogenic pressures on wildlife (**Fig. 1b**).
- A model defining zoogeographic favourability for Ebola virus presence was produced by defining mammalian chorotypes (Olivero et al. 2011); and then using the Favourability Function to build a model based on these chorotypes (**Fig. 1c**).
- The environmental and zoogeographic models were compared according to goodness of fit, classification and discrimination capacities.
- Both models were combined using fuzzy intersection (**Fig. 1d**).

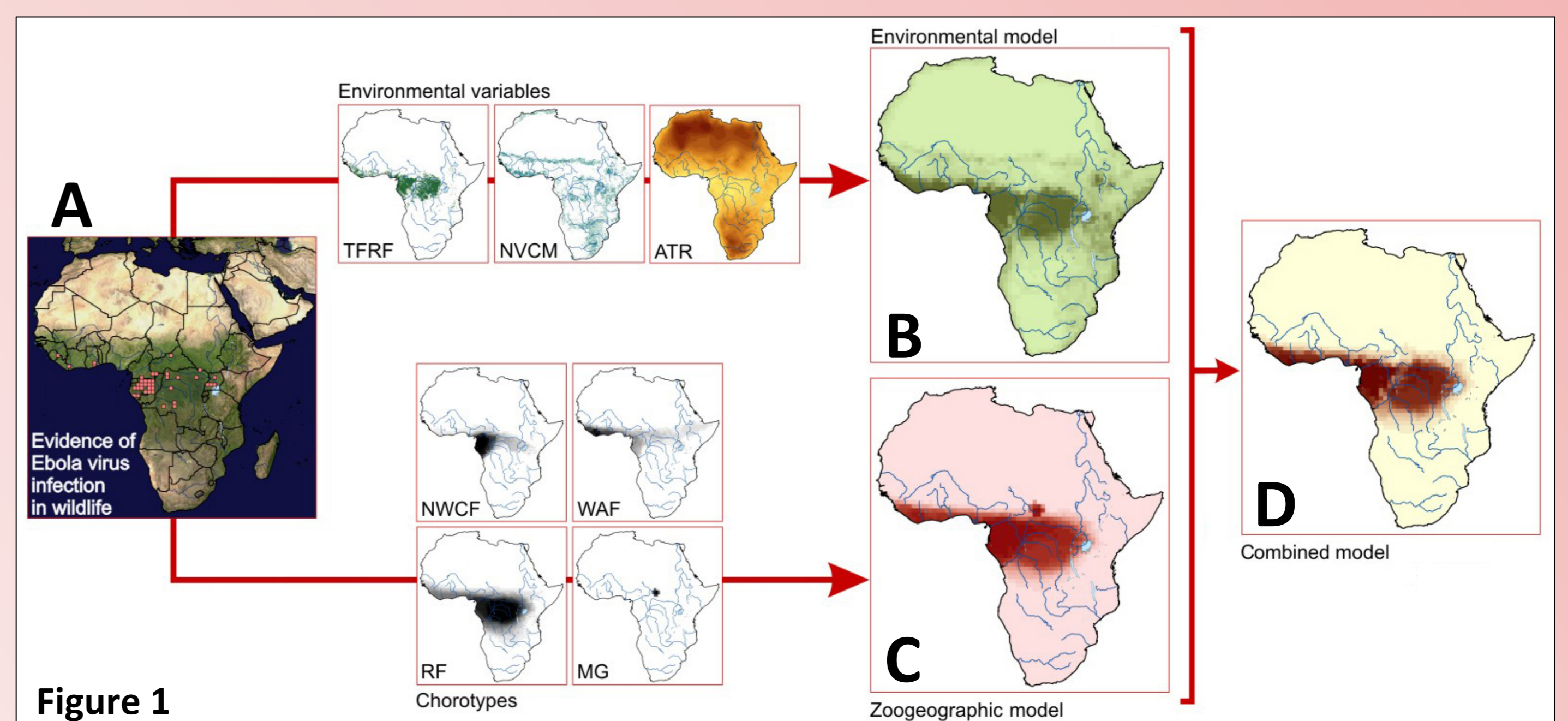**Figure 2.** Record of Ebola virus in mammals

Figure 1

RESULTS

- The environmental model of Ebola virus (**Fig. 1b**) was significantly associated with *terra-firme* rain forests (TFRF), natural vegetation/cropland mosaics (NVCM) and temperature range (ATR).
- We detected 16 significant types of mammalian distributions (**Fig. 3**). The zoogeographic model of Ebola virus (**Fig. 1c**) was associated with four chorotypes.
- The zoogeographic model showed a better goodness of fit, higher discrimination and greater classification power than the environmental model. However, both provides significant complementary information about the virus distribution.
- The combined model (**Fig. 4a**) classified correctly more than 92% of the 1°x1° squares with records of the Ebola virus. The highly favourable region included a significantly higher proportion of presences in non-human mammals (χ^2_1=6.22, P<0.05), as well as in both humans and non-human mammals (χ^2_1=8.00, P<0.01). In contrast, presences recorded only in humans were significantly located within the intermediate favourability areas (χ^2_1=19.16, P<0.001).
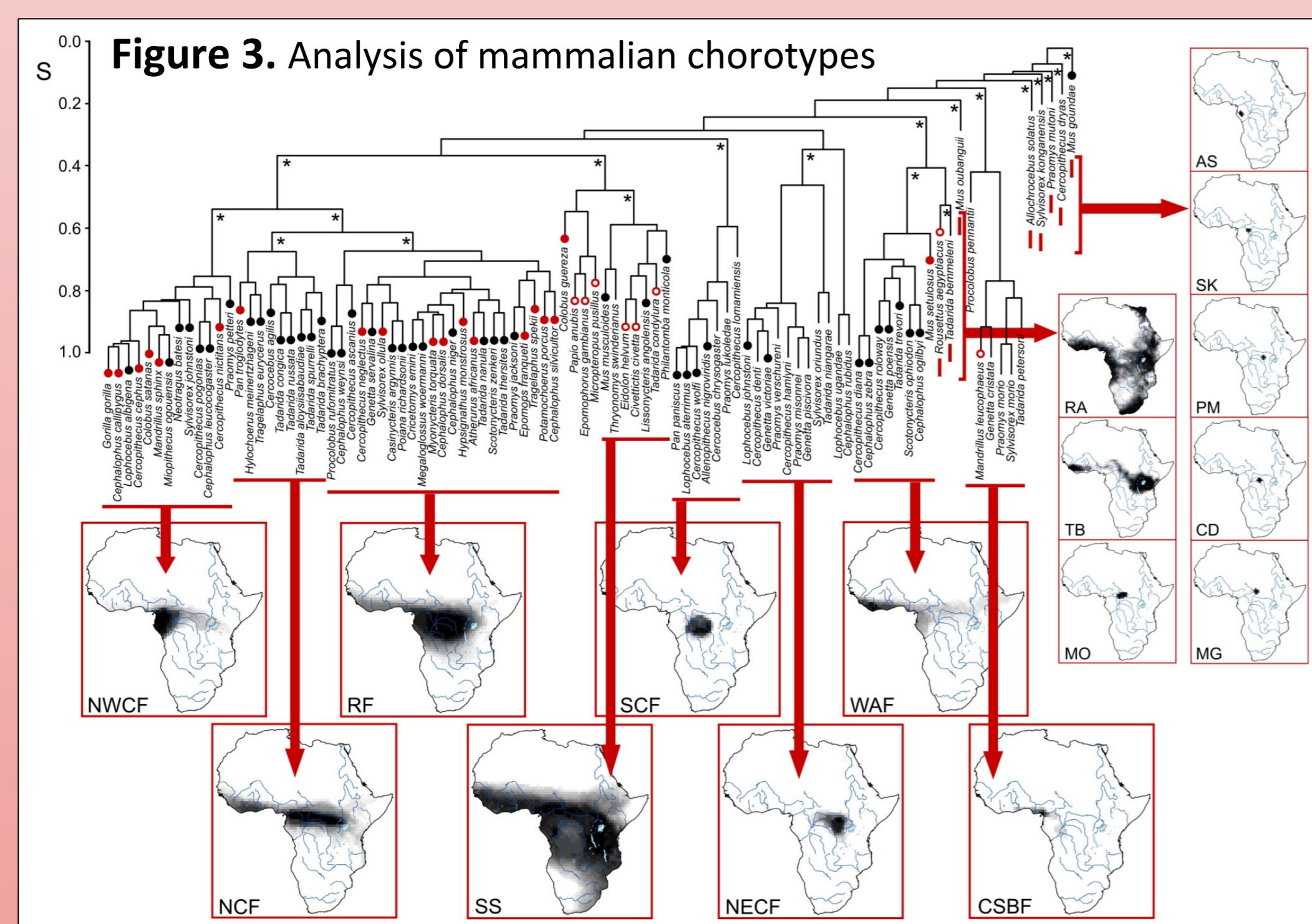- The combined model was downscaled to 0.1°×0.1° squares (**Fig. 4b**).
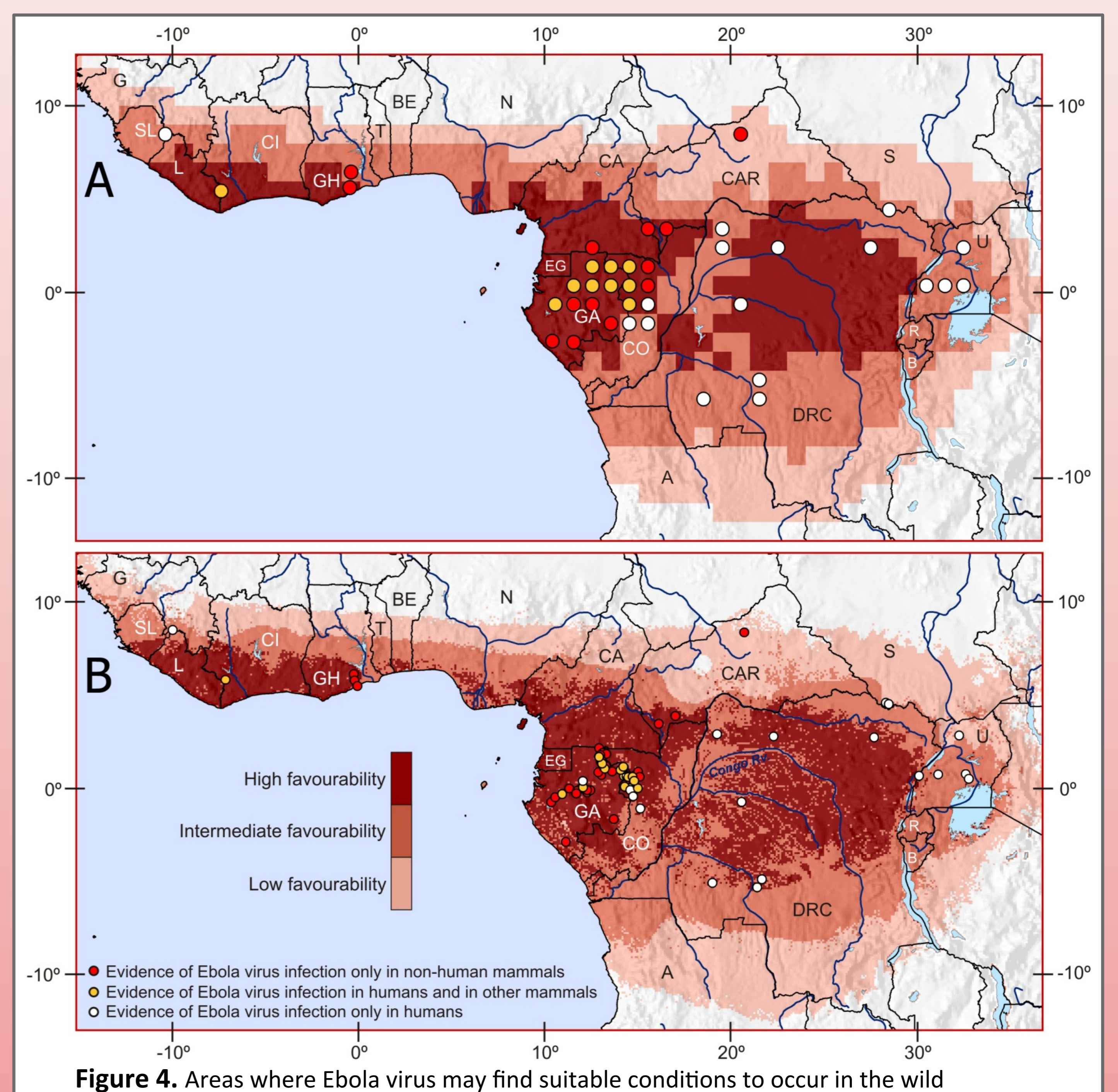

Figure 3. Analysis of mammalian chorotypes

Figure 4. Areas where Ebola virus may find suitable conditions to occur in the wild

CONCLUSIONS

- A total of 17 countries contained high favourability areas for Ebola virus (**Fig. 4b**).
- There is a significant contribution of mammalian biogeography to the distribution of Ebola virus in Africa, although vegetation may also underscore clear limits to the presence of the virus. Our model suggests that the Ebola virus distribution may be even more widespread than previously suspected, given that additional favourable areas are found throughout the coastal areas of West and Central Africa, stretching from Cameroon to Guinea, and extend further East into the East African Lakes region.
- The most favourable area for the Ebola virus could be significantly associated with the presence of the virus in animals. Such core areas are surrounded by regions of intermediate favourability in which human infections of unknown source were found. This difference in association between human and animals and the virus may offer further insights on how EVD can spread.

Cited literature

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Groseth et al. (2007) *Microbiology* 15: 408-416.
Murray et al. (2015) *PNAS* 112: 12746-12751.
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